

WHAT IS CLAIMED IS:

1. A method of determining a base sequence for nucleic acid, electrophoresing a fragment sample of nucleic acid and determining the base sequence of the nucleic acid on the basis of detected data, comprising steps of:
 - (A) performing waveform shaping by Fourier transformation on data of a certain number N of points from the head of the detected data with a parameter of a previously set peak interval;
 - (B) determining the base sequence as to data of P points ($P < N$) from the head of the data of N points;
 - (C) obtaining a peak interval from the result of the sequence determination;
 - (D) performing waveform shaping by Fourier transformation on data of N points from a position returning by L points ($L < M$) from final data precedently subjected to the sequence determination with a parameter of a precedently obtained peak interval; and
 - (E) determining the base sequence as to data of M points ($M < N$) of a central portion to be connected with data precedently subjected to the sequence determination among data of N points subjected to second or later waveform shaping, wherein
the steps (E) \rightarrow (C) \rightarrow (D) are repeated until data disappear or no analysis is required despite presence of data.
- 25 2. The method of determining a base sequence for nucleic acid according to claim 1, wherein
FFT treatment is applied as the waveform shaping by Fourier transformation.
- 30 3. The method of determining a base sequence for nucleic acid

according to claim 2, assuming that N is equal to 2^n , M is equal to $2^{(n-1)}$ and L is equal to $2^{(n-2)}$.